

SEQUENCE LISTING

<110> Deutsches Krebsforschungszentrum

<120> Use of ADAM 12 for diagnosis and therapy of preeclampsia

<130> DK62208PC

<150> EP03023815.8

<151> 2003-10-17

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<170> PatentIn version 3.1

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Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala	850		855		860
Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp	865		870		875
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348

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636

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684

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732

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828

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Asp Asn Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys						
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cag cga tta ata gag att gct aat cac gtt gac aag ttt tac aga cca						
1068						
Gln Arg Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro						
	240		245		250	
ctg aac att cgg atc gtg ttg gta ggc gtg gaa gtg tgg aat gac atg						
1116						
Leu Asn Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met						
	255		260		265	270
gac aaa tgc tct gta agt cag gac cca ttc acc agc ctc cat gaa ttt						
1164						
Asp Lys Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe						
	275		280		285	
ctg gac tgg agg aag atg aag ctt cta cct cgc aaa tcc cat gac aat						
1212						
Leu Asp Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn						
	290		295		300	
gcg cag ctt gtc agt ggg gtt tat ttc caa ggg acc acc atc ggc atg						
1260						
Ala Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met						
	305		310		315	
gcc cca atc atg agc atg tgc acg gca gac cag tct ggg gga att gtc						
1308						
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val						
	320		325		330	
atg gac cat tca gac aat ccc ctt ggt gca gcc gtg acc ctg gca cat						
1356						
Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His						
	335		340		345	350
gag ctg ggc cac aat ttc ggg atg aat cat gac aca ctg gac agg ggc						
1404						
Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly						
	355		360		365	
tgt agc tgt caa atg gcg gtt gag aaa gga ggc tgc atc atg aac gct						
1452						
Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala						
	370		375		380	

tcc acc ggg tac cca ttt ccc atg gtg ttc agc agt tgc agc agg aag
1500
Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys
385 390 395

gac ttg gag acc agc ctg gag aaa gga atg ggg gtg tgc ctg ttt aac
1548
Asp Leu Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn
400 405 410

ctg ccg gaa gtc agg gag tct ttc ggg ggc cag aag tgt ggg aac aga
1596
Leu Pro Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg
415 420 425 430

ttt gtg gaa gaa gga gag gag tgt gac tgt ggg gag cca gag gaa tgt
1644
Phe Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys
435 440 445

atg aat cgc tgc tgc aat gcc acc acc tgt acc ctg aag ccg gac gct
1692
Met Asn Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala
450 455 460

gtg tgc gca cat ggg ctg tgc tgt gaa gac tgc cag ctg aag cct gca
1740
Val Cys Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala
465 470 475

gga aca gcg tgc agg gac tcc agc aac tcc tgt gac ctc cca gag ttc
1788
Gly Thr Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe
480 485 490

tgc aca ggg gcc agc cct cac tgc cca gcc aac gtg tac ctg cac gat
1836
Cys Thr Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp
495 500 505 510

ggg cac tca tgt cag gat gtg gac ggc tac tgc tac aat ggc atc tgc
1884
Gly His Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys
515 520 525

cag act cac gag cag cag tgt gtc aca ctc tgg gga cca ggt gct aaa
1932
Gln Thr His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys
530 535 540

cct gcc cct ggg atc tgc ttt gag aga gtc aat tct gca ggt gat cct
1980
Pro Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro
545 550 555

tat ggc aac tgt ggc aaa gtc tcg aag agt tcc ttt gcc aaa tgc gag
2028
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu
560 565 570

atg aga gat gct aaa tgt gga aaa atc cag tgt caa gga ggt gcc agc
 2076
 Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser
 575 580 585 590
 cgg cca gtc att ggt acc aat gcc gtt tcc ata gaa aca aac atc ccc
 2124
 Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro
 595 600 605
 ctg cag caa gga ggc cgg att ctg tgc cgg ggg acc cac gtg tac ttg
 2172
 Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu
 610 615 620
 ggc gat gac atg ccg gac cca ggg ctt gtg ctt gca ggc aca aag tgt
 2220
 Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys
 625 630 635
 gca gat gga aaa atc tgc ctg aat cgt caa tgt caa aat att agt gtc
 2268
 Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val
 640 645 650
 ttt ggg gtt cac gag tgt gca atg cag tgc cac ggc aga ggg gtg tgc
 2316
 Phe Gly Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys
 655 660 665 670
 aac aac agg aag aac tgc cac tgc gag gcc cac tgg gca cct ccc ttc
 2364
 Asn Asn Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe
 675 680 685
 tgt gac aag ttt ggc ttt gga gga agc aca gac agc ggc ccc atc cgg
 2412
 Cys Asp Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg
 690 695 700
 caa gca gaa gca agg cag gaa gct gca gag tcc aac agg gag cgc ggc
 2460
 Gln Ala Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly
 705 710 715
 cag ggc cag gag ccc gtg gga tcg cag gag cat gcg tct act gcc tca
 2508
 Gln Gly Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser
 720 725 730
 ctg aca ctc atc tga gccctcccat gacatggaga ccgtgaccag tgctgctgca
 2563
 Leu Thr Leu Ile
 735
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 gaagtcagc 2683

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 tcaactgagcc 2863

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 agaagaaggt 3103

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 gcagtactca 3163

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 catttaacaa 3223

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 3328

<210> 4

<211> 738

<212> PRT

<213> Homo sapiens

<400> 4

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Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	Val	Ser
			20					25					30		

Leu	Trp	Asn	Glu	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	Ser	Val	Arg
		35					40					45			

Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	Ser	Lys	Asn	His
	50					55					60				

Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile
 65 70 75 80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu
 85 90 95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr
 100 105 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr
 115 120 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu
 130 135 140

Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala
 145 150 155 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg
 165 170 175

Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn
 180 185 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu
 195 200 205

Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn
 210 215 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg
 225 230 235 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn
 245 250 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys
 260 265 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp
 275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln
 290 295 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro
 305 310 315 320

Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp
 325 330 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu
 340 345 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser
 355 360 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr
 370 375 380

Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu
 385 390 395 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro
 405 410 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val
 420 425 430

Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn
 435 440 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys
 450 455 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr
 465 470 475 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr
 485 490 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His
 500 505 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr
 515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala
 530 535 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly

545		550		555		560
Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg						
	565			570		575
Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro						
	580		585		590	
Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln						
	595		600		605	
Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp						
	610		615		620	
Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp						
	625		630		635	640
Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly						
		645		650		655
Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn						
		660		665		670
Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp						
	675		680		685	
Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala						
	690		695		700	
Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly						
	705		710		715	720
Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr						
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Leu Ile

<210> 5

<211> 2642

<212> DNA

<213> Homo sapiens

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 agaagaccac 120
 cattgaaaaa ctaagggtgtg tgcgcccttc ccggccaccc cgtggcttcc
 aaccctgtca 180
 ggctcacctc ggccaccttg gaaaaggcct gatgaggaag ccgccagatt
 cctaccaccc 240
 gaaggacaat cccaggagat tgctgcagtg tcagaatgtt gacatcagca
 gaccctcaa 300
 cggcctgaat gtccttcagc cccagtcaac tcagcgagtg cttcctcccc
 tccaccgggc 360
 cccacgtgca cctagcgtcc ctgccagacc cctgccagcc aagcctgcac
 ttaggcaggc 420
 ccaggggacc tgtaagcaa accccctca gaagcctctg cctgcagatc
 ctctggccag 480
 aacaactcgg ctcaactcatg ccttggccag gaccccagga caatgggaga
 ctgggtccg 540
 cctggcaccc ctccagacctg ctccacaata tccacaccaa gtgcccagat
 ccacccacac 600
 cgcctatatt aagtgagaag ccgacacctt ttttcaacag tgaagacaga
 agtttgact 660
 atctttcagc tccagttgga gttttttgta ccaactttta ggattttttt
 taatgtttaa 720
 aacatcatta ctataagaac tttgagctac tgccgtcagt gctgtgctgt
 gctatggtgc 780
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 gattacagt 840
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aaaaaaaaaa 2640

aa
2642

<210> 6

<211> 205

<212> PRT

<213> Homo sapiens

<400> 6

Asp Asn Gln Gly Leu Thr Ile Gly Ile Leu Val Thr Ile Leu Cys Leu
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20 25 30

Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val
35 40 45

Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu
50 55 60

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro
65 70 75 80

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile
85 90 95

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln
100 105 110

Arg Val Leu Pro Pro Leu His Arg Ala Pro Arg Ala Pro Ser Val Pro
115 120 125

Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr

130	135	140
Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala		
145	150	155 160
Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp		
	165	170 175
Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln Tyr Pro		
	180	185 190
His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys		
	195	200 205

<210> 7

<211> 908

<212> DNA

<213> Homo sapiens

<400> 7

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catgacatgg 120

agaccgtgac cagtgtgct gcagaggagg tcacgcgtcc ccaaggcctc
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cagcattgac tctgtggctt tgccatcggt tccatgacaa cagacacaac
acagttctcg 240

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caaggaaggg 300

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tgctcctgag 360

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agaggactca 420

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ctctggctgc 540

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ggttttagtt 600

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tgaatggcat 660

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acatgcgtga ccagcagtac tcaggtttga gggtttgcag aaagccaggg
aaccacaga 780

gtcaccaacc cttcatttaa caagtaagaa tgttaaaaag tgaaaacaat
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aaaaaaaa
908

<210> 8

<211> 34

<212> PRT

<213> Homo sapiens

<400> 8

Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly
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Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr
20 25 30

Leu Ile

<210> 9

<211> 23

<212> DNA

<213> Homo sapiens

<400> 9

cctgtgacct ccagagttc tgc
23

<210> 10

<211> 23

<212> DNA

<213> Homo sapiens

<400> 10

gaattcctat ggtaaactc tgg
23

<210> 11

<211> 24

<212> DNA

<213> Homo sapiens

<400> 11

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24

<210> 12

<211> 24

<212> DNA

<213> Homo sapiens

<400> 12

agttgactgg ggctgagggg catt
24

<210> 13

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (15)..(15)

<223> Mismatch (g instead of c)

<400> 13
ggactctgca gcttgctgcc ttg
23

<210> 14

<211> 23

<212> DNA

<213> Homo sapiens

<400> 14
ggactctgca gcttcctgcc ttg
23

<210> 15

<211> 21

<212> DNA

<213> Homo sapiens

<400> 15
tcggggctca ggaggggaag t
21

<210> 16

<211> 21

<212> DNA

<213> Homo sapiens

<400> 16
ggctgccaag gcggaggtgt c
21

<210> 17

<211> 24

<212> DNA

<213> Homo sapiens

<400> 17
ggccgggtga tctttggtct cttc
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<210> 18

<211> 24

<212> DNA

<213> Homo sapiens

<400> 18
cccggctgtc tgtcttgggtg ctct
24

<210> 19

<211> 21

<212> DNA

<213> Homo sapiens

<400> 19
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21

<210> 20

<211> 21

<212> DNA

<213> Homo sapiens

<400> 20
ttcaggataa tcacctgagc a
21